

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 7, 2002, 16:05:23 : Search time 77.81 Seconds

(without alignments)  
25.917 Million cell updates/sec

Title: US-08-569-749-5

Sequence: 1 CELYRMSTYSTFPAQVPSVSE.....KYKFCGGLMDNWKIGDSP 55

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 3664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1          | 307   | 100.0       | 618    | 1     | BIR3_HUMAN  |
| 2          | 301   | 98.0        | 604    | 1     | BIR2_HUMAN  |
| 3          | 291   | 94.8        | 612    | 1     | BIR3_MOUSE  |
| 4          | 284   | 92.5        | 600    | 1     | BIR2_MOUSE  |
| 5          | 247   | 80.5        | 611    | 1     | BIR_CHICK   |
| 6          | 159   | 51.8        | 497    | 1     | BIR4_HUMAN  |
| 7          | 153   | 49.8        | 496    | 1     | BIR4_MOUSE  |
| 8          | 152   | 49.5        | 496    | 1     | BIR4_RAT    |
| 9          | 140   | 45.6        | 358    | 1     | PIAP_PIG    |
| 10         | 134   | 43.6        | 1402   | 1     | BIRG_MOUSE  |
| 11         | 134   | 43.6        | 1403   | 1     | BIRE_MOUSE  |
| 12         | 133   | 43.3        | 1403   | 1     | BIRF_MOUSE  |
| 13         | 132   | 43.0        | 268    | 1     | IAPF_NPYOP  |
| 14         | 127   | 41.4        | 438    | 1     | IAP1_DROME  |
| 15         | 125   | 40.7        | 1403   | 1     | BIR1_HUMAN  |
| 16         | 119   | 39.7        | 1447   | 1     | BIRB_MOUSE  |
| 17         | 112   | 38.8        | 239    | 1     | ZPP_IRV6    |
| 18         | 109   | 35.5        | 1403   | 1     | BIRA_MOUSE  |
| 19         | 103.5 | 33.7        | 275    | 1     | IAP_GYCP    |
| 20         | 102   | 33.2        | 498    | 1     | IAP2_DROME  |
| 21         | 93    | 30.3        | 275    | 1     | IAP1_NPYOP  |
| 22         | 83.5  | 27.2        | 286    | 1     | IAP1_ASFB7  |
| 23         | 75    | 24.4        | 224    | 1     | BIR5_HUMAN  |
| 24         | 73.5  | 23.9        | 142    | 1     | BIR5_MOUSE  |
| 25         | 72.5  | 23.6        | 997    | 1     | BIR1_SCHRO  |
| 26         | 71.5  | 23.3        | 4829   | 1     | BIR6_HUMAN  |
| 27         | 70.5  | 23.0        | 140    | 1     | BIR5_MOUSE  |
| 28         | 68.5  | 22.3        | 224    | 1     | IAP1_ASFB3  |
| 29         | 68.5  | 22.3        | 224    | 1     | IAP1_ASFB4  |
| 30         | 68.5  | 22.3        | 224    | 1     | IAP1_ASFB1  |
| 31         | 68.5  | 22.3        | 238    | 1     | IAP1_ASFB2  |
| 32         | 61.5  | 20.0        | 142    | 1     | BIR3_RAT    |
| 33         | 60    | 19.5        | 1401   | 1     | WRN_MOUSE   |

|    |      |      |      |   |            |                    |
|----|------|------|------|---|------------|--------------------|
| 34 | 57   | 18.6 | 707  | 1 | ORC1_SCHPO | P54789 schizosacch |
| 35 | 56   | 18.2 | 249  | 1 | IAP2_NPYAC | P41454 autographa  |
| 36 | 56   | 18.2 | 1432 | 1 | WRN_HUMAN  | Q14191 homo sapien |
| 37 | 54.5 | 17.8 | 438  | 1 | YMY6_CABEL | P34508 caenorhabdi |
| 38 | 54.5 | 17.8 | 954  | 1 | BIR1_YEAST | P47134 saccharomyc |
| 39 | 54.5 | 17.8 | 1192 | 1 | METH_MYCTU | O33259 mycobacteri |
| 40 | 53.5 | 17.4 | 949  | 1 | IF2_HLEPU  | Q92466 helicobacte |
| 41 | 53.5 | 17.4 | 1025 | 1 | HIRA_FUDRU | O42611.fugu rubrip |
| 42 | 52.5 | 17.1 | 914  | 1 | GUX2_GLOSU | P50900 clostridium |
| 43 | 52   | 16.9 | 264  | 1 | FTSO_STRCU | O60308 streptomyce |
| 44 | 52   | 16.9 | 982  | 1 | ENV_STF3L  | P27399 staphylococ |
| 45 | 51.5 | 16.8 | 244  | 1 | Y28K_SSV1  | P20213 sulfolobus  |

ALIGNMENTS

RESULT 1  
BIR3\_HUMAN STANDARD: PRT: 618 AA.  
AC Q13490: Q16516:  
DF 01-NOV-1997 (Rel. 35, Created)  
DF 01-NOV-1997 (Rel. 35, Last sequence update)  
DF 20-AUG-2001 (Rel. 40, Last annotation update)  
DE BACULOVIRAL IAP REPEAT-CONTAINING PROTEIN 3 (INHIBITOR OF APOPTOSIS  
DE PROTEIN 2) (IAP HOMOLOG B).  
DE BIR3 OR A212 OR IAP2 OR MIBB.  
CM Homo sapiens (human).  
CS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Eukaryota; Metazoa; Chordata; Carnivora; Hominoidea; Homo.  
OC Kribia; Taxid:9606;  
OX Kribia; Taxid:9606;  
RN [1]  
RX MEDLINE-96128127; PubMed-8548910;  
RA Kothé M., Pan M.G., Henzel W.J., Ayres T.M., Goeddel D.V.;  
RT "The TNFR2-TRAF signaling complex contains two novel proteins related  
RT to baculoviral inhibitor of apoptosis proteins".  
RL Cell 83:1243-1252(1995).  
RN [2]  
RX MEDLINE-96149249; PubMed-8552191;  
RA Laktion P., Roy N., Tamai K., Lefebvre C., Baird S., Chertont-Horvat G.,  
RA Farahani R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.;  
RT "Suppression of apoptosis in mammalian cells by NAIP and a related  
RT family of IAP genes".  
RL Nature 379:349-353(1996).  
RN [3]  
RX MEDLINE-96209843; PubMed-8643514;  
RA Juen A.G., Pakusch M., Hawkins C.J., Puls K.L., Vaux D.L.;  
RT "Cloning and expression of apoptosis inhibitory protein homologs that  
RT function to inhibit apoptosis and/or bind tumor necrosis factor  
RT receptor-associated factors".  
RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).  
RN [4]  
RX MEDLINE-96332054; PubMed-10404221;  
RA Hines A.G., Norton R.S., Vaux D.L., Day C.L.;  
RT "Solution structure of a baculoviral inhibitor of apoptosis (IAP)  
RT repeat...".  
RL Nat. Struct. Biol. 6:648-651(1999).  
CC -1- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS  
CC WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO  
CC FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR  
CC NECROSIS FACTOR RECEPTOR 2 (TNFR2).  
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).  
CC MAINLY EXPRESSED IN ADULT SKELETAL MUSCLE, THYMUS, TESTIS, OVARY,  
CC AND PANCREAS, LOW OR ABSENT IN BRAIN AND PERIPHERAL BLOOD  
CC LEUCOCYTES.

```

CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -----
CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: L49431; AAC41943.1; -
CC EMBL: U45879; AAC50372.1; -
CC EMBL: U37547; AAC50508.1; -
CC PDB: 1Q8H; 20-OCT-99.
CC MIM: 601723; -
CC InterPro: IPR001370; BIR.
CC InterPro: IPR001315; CARD.
CC InterPro: IPR001841; znf_fing.
CC Pfam: PF00653; BIR. 3.
CC Pfam: PF00619; CARD. 1.
CC Pfam: PF00097; zf-C3HC4; 1.
CC SMART: SM00238; BIR. 3.
CC SMART: SM00184; RING. 1.
CC SMART: SM01282; BIR_REPEAT_1; 3.
CC PROSITE: PS0143; BIR_REPEAT_2; 3.
CC PROSITE: PS0209; CARD. 1.
CC Apoptosis: zinc-finger; Repeat; 3D-structure.
CC REPEAT 46 113 BIR 1.
CC REPEAT 184 250 BIR 2.
CC REPEAT 289 336 BIR 3.
CC DOMAIN 453 539 CARD.
CC ZN_FING 571 605 RING-TYPE.
CC CONFLICT 157 157 S -> P (IN REF. 2).
CC CONFLICT 308 308 S -> G (IN REF. 2).
CC CONFLICT 414 414 Q -> L (IN REF. 2).
CC CONFLICT 514 514 L -> W (IN REF. 2).
CC SEQUENCE 618 AA: 69899 MW: C177B0328003586D CMC64;

Query Match 100.0%; Score 307; DB 1; Length 618;
Best Local Similarity 100.0%; Pred. No. 1; Se-32;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CELYRSTYSTFPAGVSESLRAGEFYTGVDNRYKCFCCGLMDNMLGDSF 55
DB 45 CELYRSTYSTFPAGVSESLRAGEFYTGVDNRYKCFCCGLMDNMLGDSF 99

RESULT 2
BIR2_HUMAN STANDARD; PRT; 604 AA.
ID BIR2_HUMAN
AC Q13489; Q16628; Q9UP46;
DT 01-NOV-1997 (rel. 35, Created)
DT 01-NOV-1997 (rel. 35, Last sequence update)
DT 20-AUG-2001 (rel. 40, Last annotation update)
DE BACULOVIRAL IAP REPEAT-CONTAINING PROTEIN 1 (INHIBITOR OF APOPTOSIS
DE PROTEIN 1) (HARP-1) (HARP-1) (C-IAP2) (TNFR2-TNRF SIGNALING COMPLEX
DE PROTEIN 1) (IAP HOMOLOG C).
GN BIRC2 OR API1 OR IAP1 OR MHC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID:9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE:96128127; PubMed:8548810;
RA Rothe M., Pan M.-C., Henzel W.J., Ayres T.M., Goeddel D.V.;
RT "The TNFR2-TNRF signaling complex contains two novel proteins related
RT to baculoviral inhibitor of apoptosis proteins."

```

```

RL Cell 83:1243-1252(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver.
RX MEDLINE:96149249; PubMed:8552191;
RA Liston P., Roy N., Tamai K., Lefebvre C., Baird S., Chertov-Horvat G.,
RA Parshanian R., McLean M., Ikeda J., McKenzie A., Korneluk R.G.;
RT "Suppression of apoptosis in mammalian cells by NAIP and a related
RT family of IAP genes."
RL Nature 379:349-353(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Petal Liver;
RX MEDLINE:96209843; PubMed:8643514;
RA Uren A.G., Pakusch M., Hawkins C.J., Puls K.L., Vaux D.L.;
RT "Cloning and expression of apoptosis inhibitory protein homologs that
RT function to inhibit apoptosis and/or bind tumor necrosis factor
RT receptor-associated factors."
RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE:99252096; PubMed:10233894;
RA Horrevorts A.J., Fontijn R.D., van Zonneveld A.J., de Vries C.J.,
RA ten Cate J.W., Pannekoek H.;
RT "Vascular endothelial genes that are responsive to tumor necrosis
RT factor-alpha in vitro are expressed in atherosclerotic lesions,
RT including inhibitor of apoptosis protein-1, steamin, and two novel
RT genes."
RL Blood 93:3418-3431(1999).
CC -1- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS
CC WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO
CC FORM AN HETEROOLIGOMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR
CC NECROSIS FACTOR RECEPTOR 2 (TNFR2).
CC -1- SUBCELLULAR LOCATION: CYTOSOL;SMC. (POTENTIAL).
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN FETAL LUNG AND KIDNEY. IN
CC THE ADULT, EXPRESSION IS MAINLY SEEN IN LYMPHOID TISSUES,
CC INCLUDING SPLEEN, THYMUS AND PERIPHERAL BLOOD LYMPHOCYTES.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -----
CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: L49432; AAC41943.1; -
CC EMBL: U45878; AAC50371.1; -
CC EMBL: U37546; AAC50507.1; -
CC EMBL: AF070674; AAC83232.1; -
CC MIM: 601712; -
CC InterPro: IPR001370; BIR.
CC InterPro: IPR001315; CARD.
CC InterPro: IPR001841; znf_fing.
CC Pfam: PF00653; BIR. 3.
CC Pfam: PF00619; CARD. 1.
CC Pfam: PF00097; zf-C3HC4; 1.
CC SMART: SM00238; BIR. 3.
CC SMART: SM00184; RING. 1.
CC PROSITE: PS01282; BIR_REPEAT_1; 3.
CC PROSITE: PS0143; BIR_REPEAT_2; 3.
CC PROSITE: PS0209; CARD. 1.
CC Apoptosis: zinc-finger; Repeat.
CC REPEAT 29 36 BIR 1.
CC REPEAT 169 335 BIR 2.
CC REPEAT 255 322 BIR 3.
CC DOMAIN 447 525 CARD.
CC ZN_FING 557 591 RING-TYPE.

```

us-08-569-749-5.rsp

```
DR DR InterPro: IPR001315; CARD.  
DR Pfam: PF00653; BIR_3.  
DR Pfam: PP00619; CARD_1.  
DR pfam: PPO0097; zf-C3HC1_1.  
DR SMART: SMO0238; BIR_3.  
DR SMART: SMO0114; CARD_1.  
DR PROSITE: PS01282; BIR_REPEAT_1_3.  
DR PROSITE: PS50143; BIR_REPEAT_2_3.  
DR PROSITE: PS50209; CARD_1.  
KM Apoptosis: zinc-finger; Repeat.  
FT REPEAT      46   113     BIR_1.  
ET REPEAT      177    243     BIR_2.  
FT REPEAT      262    329     BIR_3.  
FT DOMAIN      447    533     CARD_  
FT ZN_FING     565    599     CARD_  
FT CONFLICT    380    380     RING-TYPE  
PT FT          E -> K (IN REF. 2).  
SO SEQUENCE     612 AA; 69676 MW; ED089D9D3C6G10D CRC64;  
  
Query Match           94.8%; Score 291; DB 1; Length 612;  
Best Local Similarity 94.5%; Pred.No. 1,ge-30;  
Matches       52; Conservative        0; No.Matches       3; Indels         0; Gaps            0;
```

```
OY              1 CEIYSRSTYSTFPAGVPVSPSLSARAGRGTYGVNDKVKPFCCGLMDNMKKGDSP 55  
Db             45 CEIKRSITSYSAFRGPVSERSISLRAGFYIVGNVDKVKCFCCGLMDNMKKGGDSP 99
```

```
RESULT 4  
BIR2_MOUSE  
ID AC 008653 STANDARD: PRF: 600 AA.  
DI DI 01-NOV-1997 (Rel. 35, Created)  
DT DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DE DE 20-AUG-2001 (Rel. 40, Last annotation update)  
DE BACKGROUND INFO: REPEAT-CONTAINING PROTEIN 2 (INHIBITOR OF APOPTOSIS  
PROTEIN 2) (MARP) (MIAP-1).  
GS BIRC2 OR AP1L OR LAPL.  
SN Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;  
MM Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
NX NCBI_TaxID=10090;  
RX [1]  
RN TISSUE=Skeletal muscle;  
RC MEDLINE=98110590; PubMed=9441758;  
RA Liston P., LeFebvre C., Fong W.G.; Xuan J.Y., Korneluk R.G.;  
RT Genomic characterization of the mouse inhibitor of apoptosis protein  
1 and 2 genes." ;  
RL Genomics 46:445-503(1997).  
RU  
CU -FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS  
WITH THE RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO  
FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR  
NECROSIS FACTOR RECEPTOR 2 (TNFR2) (BY SIMILARITY).  
CC -SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).  
CC -SIMILARITY: BELONGS TO THE INA FAMILY.  
CC -SIMILARITY: CONTAINS 3 BIR REPEATS.  
CC -SIMILARITY: CONTAINS 1 CARD DOMAIN.  
CC -SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
```

```
--  
-- THIS SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation at  
the European Bioinformatics Institute. There are no restrictions on its  
use by non-profit institutions as long as their name appears in the way  
modified and this statement is not removed. Usage by others and for commercial  
entities requires a license agreement (See http://www.isdb.ch/announce/  
or send an email to license@isdb.ch).
```

```
DR EMBL: U88908; AAC53531.1; --  
DR MGDB: MGI:1197007; Birc2.  
DR InterPro: IPR001370; BIR.
```

[illegible]



|          |  |
|----------|--|
| CC       | -  SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.   |
| CC       | -  SIMILARITY: BELONGS TO THE ITP FAMILY.  |
| CC       | -  SUPERCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).  |
| CC       | CASPASE-7 (BY SIMILARITY).   |
| CC       | -  FUNCTION: APOPTOTIC SUPPRESSOR. INHIBITOR OF CASPASE-3 AND  |
| CC       | SUBMITTER(JUN-1997) TO THE EMBL/GenBank/DDJJ databases.  |
| RL       |  |
| CC       | -----  |
| CC       | This SWISS-PROT entry is copyright. It is produced through a collaboration   |
| CC       | between the Swiss Institute of Bioinformatics and the EMBL Outstation -  |
| CC       | the European Bioinformatics Institute. There are no restrictions on its  |
| CC       | use by non-profit institutions as long as its content is in no way   |
| CC       | modified and this statement is not removed. Usage by and for commercial  |
| CC       | entities requires a license agreement (See <a href="http://www.isb-slb.ch/announce/">http://www.isb-slb.ch/announce/</a> |
| CC       | or send an email to <a href="mailto:license@isb.slb.ch">license@isb.slb.ch</a> ).  |
| CC       | -----  |
| DR       | EMBL; U6842; AAC52594.1; +   |
| DR       | EMBL; U8890; AAB58376.1; +   |
| DR       | MGI; MGI:107572; Birc4.  |
| DR       | InterPro; IPRO01370; BIR.  |
| DR       | InterPro; IPRO01841; ZnF_Fing.   |
| DR       | Pfam; PF00653; BIR_3.  |
| DR       | Pfam; PF00097; zf-C3HC4; 1.  |
| DR       | SMART; SM00238; BIR; 3.  |
| DR       | SMART; SM00184; RING; 1.   |
| DR       | PROSITE; PS01282; BIR_REPEAT_1; 3.   |
| DR       | PROSITE; PS01043; BIR_REPEAT_2; 3.   |
| KW       | Apoptosis; Zinc-finger; Repeat.  |
| FT       | REPEAT 26 .. 93      BIR 1.  |
| FT       | REPEAT 163 .. 230    BIR 2.  |
| FT       | REPEAT 264 .. 329    BIR 3.  |
| FT       | ZN_RING 449 .. 483    RING-TYPE.   |
| FT       | CONFLICT 208 .. 208    E -> K (IN REF. 2).   |
| FT       | CONFLICT 317 .. 317    E -> D (IN REF. 2).   |
| FT       | CONFLICT 322 .. 322    W -> C (IN REF. 2).   |
| FT       | CONFLICT 346 .. 346    S -> P (IN REF. 2).   |
| FT       | CONFLICT 360 .. 360    I -> L (IN REF. 2).   |
| FT       | CONFLICT 388 .. 388    C -> S (IN REF. 2).   |
| FT       | CONFLICT 449 .. 449    V -> F (IN REF. 2).   |
| FT       | CONFLICT 462 .. 462    V -> A (IN REF. 2).   |
| FT       | CONFLICT 468 .. 468    K -> N (IN REF. 2).   |
| FT       | CONFLICT 490 .. 490    K -> N (IN REF. 2).   |
| SO       | SEQUENCE 496 AA; 56079 MW; EC5FAED0799FCDD8 CRC64;   |
| QY       | 2 ELKRMSTYTFPGAVGVSESLRAGFGYYGVNDKKVCFCCGLMIDNNKLQDS 54  |
| DB       | I : : : : :   : : : : :   : : : : :   : : : : :   : : : : :  |
| DB       | 26 EFNRLLKTRVANPSSSVASVLAKAGFLYTGEEDTVOCFSCHAAIDRWQYDGS 78   |
| QY       | Matches 27; Conservative 8; Pseudomatches 18; Indels 0; Gaps 0;  |
| QY       | Query Match 49.8%; Score 133; DB 1; Length 496;  |
| QY       | Best Local Similarity 50.9%; Pred. No. 1.7e-12;  |
| QY       | Matches 27; Conservative 8; Pseudomatches 18; Indels 0; Gaps 0;  |
| RESULT 8 |  |
| ID       | BIR4_RAT   |
| AC       | O9R016; STANDARD; PRT; 496 AA.   |
| DT       | 20-AUG-2001 (Rel. 40, last sequence update)  |
| DT       | 20-AUG-2001 (Rel. 40, last annotation update)  |
| DE       | BAUOUOIRAL IAP REPEAT-CONTAINING PROTEIN 4 (INHIBITOR OF APOPTOSIS   |
| DE       | PROTEIN 3) (X-LINKED INHIBITOR OF APOPTOSIS PROTEIN) (X-LINKED IAP)  |
| DE       | (IAP HOMOLOG A) (BIRC3) (BIRC-3).  |
| GN       | BIRC4 OR API3 OR XIAP.   |
| OS       | Eukarya norvegicus (Rat).  |
| OC       | Euteleostomi; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;   |
| OC       | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  |
| OX       | NCBL_TaxId=101116;   |
| RN       | [1]  |
| RP       | SEQUENCE FROM N.A.   |
| RT       | "Rattus norvegicus X-linked inhibitor of apoptosis (Iiap3) mRNA.";   |





|    | Query Match  | Best Local Similarity | Matches | Conservative | Score | DB 1 | Pred. No. | Length | Indels | Gaps |
|----|--|-----------------------|---------|--------------|-------|------|-----------|--------|--------|------|
| QY | 2 ELYNMSTVSTFPACVGVYSERSIARAFYVTVGVNDKXKCFCCGCLMDLNKKLTDSF | 43.3%                 | 25      | 67           | 133   | 1    | 23        | 1403   | 0      | 0    |
| DB | 278 EELIMDMFKDMFQSPVAGVEALVAFGEYFATKRDYKVCSSGCGLEVMABDDDD  | 46.3%                 | 25      | 67           | 133   | 1    | 23        | 1403   | 0      | 0    |

```

RESULT 13
IAP3_NPVP STANDARD: PRT: 268 AA.
ID IAP3_NPVP
AC P41437:
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE APOPTOSIS INHIBITOR 3 (IAP-3).
GN IAP3 OR IAP.
OS Oryza latifolia multicaulis multicaulis virus (OPMNPV).
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
NC Nucleopolydnavirus.
CC NCBI_TaxId=64623;
XX NCBI_TaxId=64623;
NN (1)
RX SEQUENCE FROM N.A.
RX MEDLINE=9187094; PubMed=9139334;
RX Birdman M., O'Connell J., Miller L.K.;
RT "Amino acid sequencing of the nuclear polyhedrosis virus
RT encoding a polyhedrin-15b Cys/His sequence motifs.";
RL J. Virol. 68:2521-2528(1994).
RL [2]
RX SEQUENCE FROM N.A.
RX MEDLINE=97271300; PubMed=9126251;
RX Abrams C.H., Russell R.R., Funk C.J., Evans J., Harwood S.,
RA Rohmann G.F.;
RT "The sequence of the Oryza latifolia multicaulis nuclear
RT polyhedrosis virus genome.";
RL Virology 229:381-399(1997).
CC -1- FUNCTION: ACTS BY BLOCKING CELLULAR APOPTOSIS RATHER THAN BY
CC PREVENTING VIRAL STIMULATION OF APOPTOSIS.
CC -1- SIMILARITY: CONTAINS 2 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by for commercial
CC entities requires a license agreement (See http://www.isb-sdb.ch/announce/
CC or send an email to license@sdb-sib.ch).
CC -----
DR EMBL, L22564; AB02610.1; -.
DR EMBL, U75930; AAC59034.1; -.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001841; ZnF_fing.
DR Pfam: PF00653; BIR; 2.
DR Pfam: PF00697; ZF-CHC4; 1.
DR SMART, SM0238; BIR; 2.
DR SMART, SM00184; RING; 1.
DR -----

```

|   | DR   | PROSITE:  | P50182;                           | BIR_REPEAT_1; 2. |
|---|--|-----------|-----------------------------------|------------------|
| PS0143; <td>DR<td>PROSITE:</td><td>P50143;<td>BIR_REPEAT_2; 2.</td></td></td> | DR <td>PROSITE:</td> <td>P50143;<td>BIR_REPEAT_2; 2.</td></td> | PROSITE:  | P50143; <td>BIR_REPEAT_2; 2.</td> | BIR_REPEAT_2; 2. |
| Apoptosis1;   | DR   | PROSITE:  | Zinc-finger; Repeat.              |                  |
| FT REPEAT   | 18   |           | 84                                | BIR_1.           |
| FT REPEAT   | 111  |           | 178                               | BIR_2.           |
| FT ZN_FING  | 221  |           | 255                               | RING_TYPE        |
| SEQUENCE  | 268 AA;  | 30076 MM; | D9E9175DDEB5A708                  | CRC64_A          |

```

Query Match      43.0%; Score 132; DB 1; Length 268;
Best Local Similarity 42.6%; Pident No. 5; 2e-10;
Matches 23; Conservative 10; Mismatches 21; Indels 0; Gaps 0;

OY 2 ELYKMSYSTRFFPAGVPYSESLARAGFYFYTVNDYKXCCGGLMLNKKLQDSP 55
Db 111 EAARLRFFAEWIRPGIKORPEELALAEAFYFGQGGKTRKCCDGLKMEWDADP 164

```

| RESULT 14   | STANDARD: | PRT: | 438 AA. |
|---|-----------|------|---------|
| 1D IAP1.DROME   |           |      |         |
| AD 024306;  |           |      |         |
| DT 01-NOV-1997 (Rel. 35, Created)   |           |      |         |
| DT 01-NOV-1997 (Rel. 35, Last sequence update)  |           |      |         |
| DT 20-AUG-2001 (Rel. 40, Last annotation update)  |           |      |         |
| DE APOPTOSIS 1 INHIBITOR (INHIBITOR OF APOPTOSIS 1) (DIAP1) (THREAD PROTEIN).   |           |      |         |
| DE IAP1 OR TH.  |           |      |         |
| GN Drosophila melanogaster (fruit fly).   |           |      |         |
| OC Eukaryota; Arthropoda; Tracheata; Hexapoda; Insecta;   |           |      |         |
| OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  |           |      |         |
| OC Ephydroidea; Drosophilidae; Drosophila.  |           |      |         |
| OX NCBI_Taxid=7227;   |           |      |         |
| XX [1]  |           |      |         |
| RP SEQUENCE FROM N.A.   |           |      |         |
| RC TISSUE=Eye Imaginal disk:  |           |      |         |
| RA MEDLINE=66128128; PubMed=6548811;  |           |      |         |
| RA Hay B.A.; Wasserman D.A.; Rubin G.M.;  |           |      |         |
| RT "Drosophila homologs of baculovirus inhibitor of apoptosis proteins function to block cell death.";                      |           |      |         |
| RL Cell 83:1253-1262(1995).   |           |      |         |
| CC -1- FUNCTION: APOPTOTIC SUPPRESSOR. OVEREXPRESSION SUPPRESSES RPR AND  |           |      |         |
| CC -1- HID-DEPENDENT CELL DEATH IN THE EYE.   |           |      |         |
| CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.   |           |      |         |
| CC -1- SIMILARITY: CONTAINS 2 RING REPEATS.   |           |      |         |
| CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  |           |      |         |
| CC -----  |           |      |         |
| CC This SWISS-PROT entry is copyright. It is produced through a collaboration   |           |      |         |
| CC between the Swiss Institute of Bioinformatics and the EMBL outstation at   |           |      |         |
| CC the European Bioinformatics Institute. There are no restrictions on the  |           |      |         |
| CC use by non-profit institutions as long as its content is in no way   |           |      |         |
| CC modified and this statement is not removed. Usage by and for commercial  |           |      |         |
| CC entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> |           |      |         |
| CC or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).  |           |      |         |
| CC -----  |           |      |         |
| CC EMBL: LA9340; AAC1609.1; "   |           |      |         |
| CC InterPro: IPR0003691; tr.  |           |      |         |
| CC InterPro: IPR001370; BIR.  |           |      |         |
| CC InterPro: IPR001841; Znf_Fing.   |           |      |         |
| CC Pfam: PF00653; BIR. 2;   |           |      |         |
| CC Pfam: PF00097; zf-C3HC4.1.   |           |      |         |
| CC SMART: SM00238; BIR. 2;  |           |      |         |
| CC SMART: SM00184; RING. 1;   |           |      |         |
| CC PROSITE: PS01282; BIR.REPEAT.1; 2;   |           |      |         |
| CC PROSITE: PS0143; BIR.REPEAT.2; 2;  |           |      |         |
| CC KW APOPTOSIS; Zinc-finger; Repeat;   |           |      |         |
| CC REPEAT 44 110  |           |      |         |
| CC REPEAT 226 293 BIR. 1.   |           |      |         |
| CC FT ZN_FING 391 425 RING-TYPE   |           |      |         |
| CC SEQUENCE 438 AA; 48098 MW; A6C22C8D55AEP29 CRC64;  |           |      |         |



Best Local Similarity 42.6%, Pred. No. 3,9e-09;  
Matches 22; Conservative 8; Mismatches 23; Indels 0; Gaps 0;

OY 2 ELYMSTYSTFPAGVPSERSIARAGFTYGVNDKVKCCGGLNDKMLGDSF 55  
DB 226 ETALATFEAMRNLAKRPHOLAEAFYTGVDGRKRCFSCGGGLMDNDDEE 279

RESULT 15

BIRL HUMAN STANDARD: PRT: 1403 AA.

ID BIRL HUMAN AC 013075: 013730: 099796: 075857;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE 20-AUG-2001 (Rel. 40, Last annotation update)  
DE BACULOVIRAL IAP REPEAT-CONTAINING PROTEIN 1 (NEURONAL APOPTOSIS  
DE INHIBITORY PROTEIN).  
CN BIR1 OR NAIP  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eularchia; Primates; Catarrhini; Hominoidea; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=85112244; PubMed=7812013;  
RA Roy N., Mahadevan M.S., McLean W., Shutter G., Varaghi Z.,  
RA Farhadi R., Baird S., Besner-Johnston A., Lefebvre C., Kang X.,  
RA Salih M., Aubry H., Tamai R., Guan X., Joannou P., Crawford T.O.,  
RA de Jong P., Suth L., Ikeda J., Korneluk R.G., Mackenzie A.;  
RA The gene for neuronal apoptosis inhibitory protein is partially  
RA deleted in individuals with spinal muscular atrophy.;  
RA Cell 80:167-178(1995).  
RN [2]  
RP SEQUENCE FROM N.A., AND REVISIONS.  
RC TISSUE=Brain;  
RX MEDLINE=98163755; PubMed=9503025;  
RA Chen Q., Baird S.D., Mahadevan M., Besner-Johnston A., Farhadi R.,  
RA Yuan J.-Y., Kang X., Lefebvre C., Ikeda J.-Y., Korneluk R.G.,  
RA Mackenzie A.E.;  
RA Sequence of a 131-kb region of 5q13.1 containing the spinal muscular  
RA atrophy candidate genes SMN and NAIP.;  
RA Genomics 48:121-127(1998).  
RN [3]  
RP SEQUENCE OF 386-623 FROM N.A.  
RA der Steege G., Draaljeers T.G., Grootscholten P.M., Osinga J.,  
RA Anzeveno R., Velona I., Brahe C., Scheffer H., van Ommen G.J.B.,  
RA Buys C.H.C.M.;  
RA Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE OF 222-1403 FROM N.A.  
RA Jones K., Graves T., McPherson J.;  
RA Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP FUNCTION:  
RC TISSUE=Liver;  
RX MEDLINE=96149249; PubMed=8552191;  
RA Liston P., Roy N., Tamai R., Lefebvre C., Baird S., Cherton-Horvat G.,  
RA Farhadi R., McLean M., Ikeda J., Korneluk R.G.;  
RA Suppression of apoptosis in mammalian cells by NAIP and a related  
RA family of IAP genes.;

-1- FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF  
CC SIGNALS.  
CC -1- TISSUE SPECIFICITY: EXPRESSED IN MOTOR NEURONS, BUT NOT IN SENSORY  
CC NEURONS, FOUND IN LIVER AND PLACENTA, AND IN A LESSER EXTENT IN  
CC SPINAL CORD.

-1- DISEASE: MUTATED OR DELETED FORMS OF NAIP HAVE BEEN FOUND IN  
CC INDIVIDUALS WITH SPINAL MUSCULAR ATROPHY TYPE I (SMA TYPE I). SMAS  
CC ARE FATAL AUTOSOMAL RECESSIVE DISORDERS SUBCLASSIFIED AS TYPE I  
CC (WERDNIG-HOFFMANN DISEASE), TYPE II (INTERMEDIATE FORM), AND TYPE  
CC III (WOLFF-PARK-WIEGANDER DISEASE) BASED UPON THE AGE OF  
CC ONSET AND CLINICAL SEVERITY. THESE NEURODEGENERATIVE DISORDERS ARE

CC CHARACTERIZED BY DEGENERATION OF LOWER MOTOR NEURONS, LEADING TO  
CC PROGRESSIVE PARALYSIS MUSCULAR ATROPHY. CONCERNS 1 IN 6000  
CC MEMBERS.  
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch))

CC EMBL: U19251; AAC52045.1; -  
CC EMBL: U80017; AAC52047.1; -  
CC EMBL: U21913; AA64504.1; -  
CC EMBL: AC005031; AAC62261.1; -  
CC MIM: 600355; -  
CC INTERPRO: IPR001370; BIR.  
CC Pfam: PF00653; BIR\_3.  
CC SMART: SM00238; BIR\_3.  
CC PROSITE: PS01492; BIR\_REPEAT\_1; 3.  
CC PROSITE: PS01493; BIR\_REPEAT\_2; 3.  
CC KW Apoptosis; Repeat. 127  
FT REPEAT 60 BIR 1.  
FT REPEAT 159 227 BIR 2.  
FT REPEAT 278 345 BIR 3.  
FT CONFLICT 222 223 PR -> YR (IN REF. 4).  
FT CONFLICT 386 387 VP -> ST (IN REF. 3).  
FT CONFLICT 535 535 M -> V (IN REF. 3).  
FT CONFLICT 553 553 Y -> H (IN REF. 3).  
FT CONFLICT 1228 1231 MISSING (IN REF. 4).  
FO SEQUENCE 1403 AA; 159613 MW; 566304C154DA3E54 CRC64;

Query Match 40.7%; Score 125; DB 1; Length 1403;  
Best Local Similarity 40.7%; Pred. No. 2.3e-08;  
Matches 22; Conservative 11; Mismatches 21; Indels 0; Gaps 0;  
OY 2 ELYMSTYSTFPAGVPSERSIARAGFTYGVNDKVKCCGGLNDKMLGDSF 55  
DB 278 EBLRDSKDPRESAVNALAKGLTYGIDVOCFSCGGCLERKMBDDP 331

Search completed: January 7, 2002, 16:05:24  
Job time: 1403 sec

.....

---